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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=10; day=27; hr=15; min=2; sec=33; ms=739;]

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Reviewer Comments:

<210> 12

<211> 42

<212> DNA

<213> Primer

<220>

<221> misc_feature

<222> (1)..(42)

<223> gag-mut1-rneu

<400> 12

aattaagagc tccacgtctc ccccccgtaa cagcaactgg cg

42

Numeric Identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." For all sequences using "Unknown or Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. Suggest using "Artificial sequence" for numeric identifier <213> and "Primer" for numeric identifier <223> in the mandatory feature. Please check for similar errors and make all necessary changes.

Application No: 10528748 Version No: 2.0

Input Set:

Output Set:

Started: 2009-10-02 17:59:46.687
Finished: 2009-10-02 17:59:50.610
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 923 ms
Total Warnings: 2
Total Errors: 32
No. of SeqIDs Defined: 40
Actual SeqID Count: 40

Error code	Error Description
E 356	Organism is not permitted in <213> in SEQ ID (12)
E 356	Organism is not permitted in <213> in SEQ ID (13)
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E 356	Organism is not permitted in <213> in SEQ ID (18)
E 356	Organism is not permitted in <213> in SEQ ID (19)
E 356	Organism is not permitted in <213> in SEQ ID (20)
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E 356	Organism is not permitted in <213> in SEQ ID (22)
E 356	Organism is not permitted in <213> in SEQ ID (23)
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E 356	Organism is not permitted in <213> in SEQ ID (27)
E 356	Organism is not permitted in <213> in SEQ ID (28)
E 356	Organism is not permitted in <213> in SEQ ID (29)
E 356	Organism is not permitted in <213> in SEQ ID (30)
E 356	Organism is not permitted in <213> in SEQ ID (31)

Input Set:

Output Set:

Started: 2009-10-02 17:59:46.687
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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 311	Invalid field content in <220> in SEQ ID (40)
E 249	Order Sequence Error <220> -> <211>; Expected Mandatory Tag: <400> in SEQID (40)
W 402	Undefined organism found in <213> in SEQ ID (40)
W 333	tabs used in amino acid numbering SEQID (40)
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH
<120> Vaccine against Oncovirus Infections, such as infections by
Feline leukosis virus of the cat
<130> XI 1292-03
<150> DE 102 44 863.9
<151> 2002-09-23
<160> 40
<170> PatentIn version 3.3
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<212> DNA
<213> Feline leukemia virus

<220>
<221> gene
<222> (1)..(1929)
<223> DNA sequence wild type "env" gene without signal peptide coding
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<308> NCBI M12500
<309> 2001-02-21
<313> (162)..(1990)

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tctatgttag gaaccttaac cgatgcctac cctaccctac atgttgactt atgtgaccta 240
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 <213> Feline leukemia virus

<220>
 <221> gene
 <222> (1)..(1527)
 <223> DNA sequence wild type "gag" gene

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<210> 3
<211> 642
<212> PRT
<213> Feline leukemia virus

<220>
<221> PEPTIDE
<222> (1)...(447)
<223> Amino acid sequence of the protein corresponding to Seq.ID1

<400> 3

Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu Ser
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Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp Ile Gly
20 25 30

Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr Trp Val Ile
35 40 45

Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr Ser Met Leu Gly
50 55 60

Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val Asp Leu Cys Asp Leu
65 70 75 80

Val Gly Asp Thr Trp Glu Pro Ile Val Leu Asn Pro Thr Asn Val Lys
85 90 95

His Gly Ala Arg Tyr Ser Ser Lys Tyr Gly Cys Lys Thr Thr Asp
100 105 110

Arg Lys Lys Gln Gln Thr Tyr Pro Phe Tyr Val Cys Pro Gly His
115 120 125

Ala Pro Ser Leu Gly Pro Lys Gly Thr His Cys Gly Ala Gln Asp
130 135 140

Gly Phe Cys Ala Ala Trp Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp
145 150 155 160

Lys Pro Thr Ser Ser Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser
165 170 175

Gln Asp Asn Ser Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe
180 185 190

Thr Gln Lys Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly

195

200

205

Leu Arg Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val
210 215 220

Ser Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
225 230 235 240

Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly
245 250 255

Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg
260 265 270

Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly Thr Gly Asp
275 280 285

Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala Leu Asn Ala Thr
290 295 300

Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro
305 310 315 320

Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr
325 330 335

Asn Pro Pro Pro Ser Cys Leu Ser Thr Pro Gln His Lys Leu Thr Ile
340 345 350

Ser Glu Val Ser Gly Gln Gly Met Cys Ile Gly Thr Val Pro Lys Thr
355 360 365

His Gln Ala Leu Cys Asn Lys Thr Gln Gln Gly His Thr Gly Ala His
370 375 380

Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu
385 390 395 400

Thr Pro Cys Ile Ser Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys
405 410 415

Val Leu Ile Glu Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr
420 425 430

Val Tyr Thr His Phe Ala Lys Ala Val Arg Phe Arg Arg Glu Pro Ile
435 440 445

Ser Leu Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile
450 455 460

Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
465 470 475 480

Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu Glu
485 490 495

Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser Glu Val
500 505 510

Val Leu Gln Asn Arg Arg Gly Leu Asp Ile Leu Phe Leu Gln Glu Gly
515 520 525

Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ala Asp His
530 535 540

Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu Arg Glu Arg Leu Lys
545 550 555 560

Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln Gly Trp Phe Glu Gly Trp
565 570 575

Phe Asn Lys Ser Pro Trp Phe Thr Thr Leu Ile Ser Ser Ile Met Gly
580 585 590

Pro Leu Leu Ile Leu Leu Ile Leu Leu Phe Gly Pro Cys Ile Leu
595 600 605

Asn Arg Leu Val Gln Phe Val Lys Asp Arg Ile Ser Val Val Gln Ala
610 615 620

Leu Ile Leu Thr Gln Gln Tyr Gln Ile Lys Gln Tyr Asp Pro Asp
625 630 635 640

Arg Pro

<210> 4
<211> 508
<212> PRT
<213> Feline leukemia virus

<220>
<221> PEPTIDE
<222> (1)..(508)
<223> Amino acid sequence of the protein corresponding to Seq.ID2

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1 5 10 15

Ser Glu Val Gln Ala Arg Ala Arg Asn Gln Gly Val Glu Val Arg Lys
20 25 30

Lys Lys Trp Ile Thr Leu Cys Glu Ala Glu Trp Val Met Met Asn Val
35 40 45

Gly Trp Pro Arg Glu Gly Thr Phe Thr Ile Asp Asn Ile Ser Gln Val
50 55 60

Glu Glu Arg Ile Phe Ala Pro Gly Pro Tyr Gly His Pro Asp Gln Ile
65 70 75 80

Pro Tyr Ile Thr Thr Trp Arg Ser Leu Ala Thr Asp Pro Pro Pro Trp
85 90 95

Val Arg Pro Phe Leu Pro Pro Pro Lys His Pro Arg Thr Asp Pro Pro
100 105 110

Glu Pro Leu Ser Pro Gln Pro Leu Ala Pro Gln Pro Ser Ser Pro His
115 120 125

Pro Val Leu Tyr Pro Val Leu Pro Lys Pro Asp Pro Pro Lys Ala Pro
130 135 140

Val Leu Pro Pro Asn Pro Ser Ser Pro Leu Ile Asp Leu Leu Thr Glu
145 150 155 160

Glu Pro Pro Pro Tyr Pro Gly Gly His Gly Pro Thr Pro Pro Ser Gly
165 170 175

Pro Arg Thr Pro Thr Ala Ser Pro Ile Ala Ile Arg Leu Arg Glu Arg
180 185 190

Arg Glu Asn Pro Ala Glu Lys Ser Gln Ala Leu Pro Leu Arg Glu Asp
195 200 205

Pro Asn Asn Arg Pro Gln Tyr Trp Pro Phe Ser Ala Ser Asp Leu Tyr
210 215 220

Asn Trp Lys Leu His Asn Pro Pro Phe Ser Gln Asp Pro Val Ala Leu
225 230 235 240

Thr Asn Leu Ile Glu Ser Ile Leu Val Thr His Gln Pro Thr Trp Asp
245 250 255

Asp Cys Gln Gln Leu Leu Gln Ala Leu Leu Thr Ala Glu Glu Arg Gln
260 265 270

Arg Val Leu Leu Glu Ala Arg Lys Gln Val Pro Gly Glu Asp Gly Arg
275 280 285

Pro Thr Gln Leu Pro Asn Val Val Asp Glu Ala Phe Pro Leu Thr Arg
290 295 300

Pro Asn Trp Asp Phe Cys Thr Pro Ala Gly Arg Glu His Leu Arg Leu
305 310 315 320

Tyr Arg Gln Leu Leu Ala Gly Leu Arg Gly Ala Ala Arg Arg Pro
325 330 335

Thr Asn Leu Ala Gln Val Lys Gln Val Val Gln Gly Lys Glu Glu Thr
340 345 350

Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu Ala Tyr Arg Met Tyr Thr
355 360 365

Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala Ala Ser Val Ile Leu Ser
370 375 380

Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg Asn Lys Leu Gln Arg Leu
385 390 395 400

Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp Leu Leu Lys Glu Ala Glu
405 410 415

Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu Glu Arg Glu Glu Arg Leu
420 425 430

Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys Arg His Lys Glu Met Thr
435 440 445

Lys Val Leu Ala Thr Val Val Ala Gln Asn Arg Asp Lys Asp Arg Gly
450 455 460

Glu Ser Lys Leu Gly Asp Gln Arg Lys Ile Pro Leu Gly Lys Asp Gln
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Cys Ala Tyr Cys Lys Glu Lys Gly His Trp Val Arg Asp Cys Pro Lys
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Arg Pro Arg Lys Lys Pro Ala Asn Ser Thr Leu Leu
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<210> 5
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<212> DNA
<213> Feline leukemia virus

<220>
<221> misc_feature
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<223> DNA sequence of the mutagenized "gag" gene

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gccgagtgcc tcatatgatgaa cgtgggtcg cccaggagg gcacccatcac catcgacaac 180
atcagccagg tggaggagag gatcttcgccc cccggcccc acggccaccc cgaccagatc 240
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 <212> PRT
 <213> Feline leukemia virus

<220>
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 <222> (1)..(509)
 <223> Amino acid sequence of the protein corresponding to Seq.ID5

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35 40 45

Gly Trp Pro Arg Glu Gly Thr Phe Thr Ile Asp Asn Ile Ser Gln Val
50 55 60

Glu Glu Arg Ile Phe Ala Pro Gly Pro Tyr Gly His Pro Asp Gln Ile
65 70